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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/781,564	02/18/2004	James P. Quigley	1361.036US1	9290

21186 7590 12/05/2006

SCHWEGMAN, LUNDBERG, WOESSNER & KLUTH, P.A.
P.O. BOX 2938
MINNEAPOLIS, MN 55402

EXAMINER

SANG, HONG

ART UNIT PAPER NUMBER

1643

DATE MAILED: 12/05/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary

Application No.

10/781,564

Applicant(s)

QUIGLEY ET AL.

Examiner

Hong Sang

Art Unit

1643

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 01 November 2006.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 1 and 32 is/are pending in the application.
- 4a) Of the above claim(s) _____ is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☐ Claim(s) 1 and 32 is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on _____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
- ☐ Certified copies of the priority documents have been received.
 - ☐ Certified copies of the priority documents have been received in Application No. _____.
 - ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- | | |
|--|---|
| 1) <input type="checkbox"/> Notice of References Cited (PTO-892) | 4) <input type="checkbox"/> Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____ |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948) | 5) <input type="checkbox"/> Notice of Informal Patent Application |
| 3) <input type="checkbox"/> Information Disclosure Statement(s) (PTO/SB/08)
Paper No(s)/Mail Date _____ | 6) <input checked="" type="checkbox"/> Other: <u>Exhibits A, B and C</u> . |

DETAILED ACTION

RE: Quigley et al

1. Applicant's response filed on 11/1/2006 is acknowledged. Claims 1 and 32 are pending. Claims 2-31 and 33 are cancelled.
2. Claims 1 and 32 are under examination.
3. The text of those sections of Title 35, U.S. Code not included in this action can be found in a prior Office action.
4. Applicants noted in the response that "the sequence alignments: Exhibits A and B" could not be located in the previous office action. Copies of the Exhibits A and B are therefore attached hereto. The Exhibits A and B can also be found in the PAIR (they were scanned on 5/5/06 but were misplaced under Document Type "Examiner's Search Strategy", see pages 13, 15 and 17).

Objections Withdrawn

5. The objection to the specification because the Brief Description of the Drawings does not reference each of the Figures is withdrawn in view of applicant's amendment to the specification.

Rejections Withdrawn

6. The rejection of claims 1, 2, 31 and 32 under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter is withdrawn in view of applicant's amendment to the claims.

7. The rejection of claims 2 and 31 under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement is withdrawn in view of applicant's cancellation of the claims.

8. The rejection of claims 2, 31 and 32 under 35 U.S.C. 102(b) as being anticipated by WO 02/04508 A1 (Pub. Date: 1/17/2002, IDS) is withdrawn in view of applicants amendment to claim 32 and cancellation of claims 2 and 31.

9. The rejection of claims 2, 31 and 32 under 35 U.S.C. 102(e) as being anticipated by Schweifer et al. (US20020142003A1, effective filing date at least 7/6/2001) is withdrawn in view of applicants amendment to claim 32 and cancellation of claims 2 and 31.

New Grounds of Rejections

10. Claim 32 is rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. This is a **new matter** rejection.

The term "provided that the combination is not arginine (525), glycine (709), and serine (827); or glutamine (525), glycine (709), and asparagines (827); or glutamine (525), aspartic acid (709) and asparagines (827)." is considered new matter since the

specification, drawings and claims as filed disclose only the amino acid sequence of SEQ ID NO.1, and the variant of SEQ ID NO.1, wherein the variant has an amino acid 525 either arginine or glutamine, has an amino acid 709 either glucine or aspartic acid, and has an amino acid 827 either serine or asparagines (see original claim 32, page 10, last paragraph and page 33, lines 1-5). There is no clear support for a variant of SEQ ID NO.1 that is not arginine (525), glycine (709), and serine (827); or glutamine (525), glycine (709), and asparagines (827); or glutamine (525), aspartic acid (709) and asparagines (827).

Applicant is required to cancel the new matter in the reply to this Office Action.

11. Claim 1 is rejected under 35 U.S.C. 102(b) as being anticipated by Scherl-Mostageer et al. (Oncogene, 2001, 20: 4402-4408, IDS).

Claim 1 is drawn to an isolated protein having SEQ ID NO.1 that is glycosylated or non-glycosylated.

Scherl-Mostageer et al. teach an isolated protein having a sequence shown in Figure 2. While the sequence shown in Figure 2 is not 100% identical to the instant SEQ ID NO.1 (there is one amino acid difference at position 827), this sequence was replaced (corrected) on 3/7/2006 by a sequence that is 100% identical to the instant SEQ ID NO.1 (see sequence alignment Exhibit C). Because Sherl-Mostageer et al. teach the very same protein, the teachings of Sherl-Mostageer et al. anticipate the instant claim.

"The discovery of a previously unappreciated property of a prior art composition, or of a scientific explanation for the prior art's functioning, does not render the old composition patentably new to the discoverer." Atlas Powder Co. v. Ireco Inc., 190 F.3d 1342, 1347, 51 USPQ2d 1943, 1947 (Fed. Cir. 1999). Thus the claiming of a new use, new function or unknown property which is inherently present in the prior art does not necessarily make the claim patentable. In re Best, 562 F.2d 1252, 1254, 195 USPQ 430, 433 (CCPA 1977). In In re Crish, 393 F.3d 1253, 1258, 73 USPQ2d 1364, 1368 (Fed. Cir. 2004). See MPEP 2112.

Conclusion

12. No claims are allowed.
13. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Hong Sang whose telephone number is (571) 272 8145. The examiner can normally be reached on 8:30am-5:00pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Larry R. Helms can be reached on (571) 272-0832. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should

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you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

Hong Sang, Ph.D.
Art Unit 1643
Dec. 1, 2006

A handwritten signature in black ink, appearing to be 'L. Helms', written in a cursive style.

LARRY R. HELMS, PH.D.
SUPERVISORY PATENT EXAMINER

XX
AC AAM9641;XX
DT 17-MAY-2002 (E1sec entry)XX
DE Human tumour-associated antigen B345 protein SEQ ID NO 4.XX
XX Tumour-associated antigen; human; B345; cytostatic; cell communication;XX
KM cell interaction; signal transduction; metastasis; cancer; colon;XX
KM immunotherapy; carcinoma; lung; diagnosis.XX
OS Homo sapiens.XX
XX NCBI: 2002-0002XX
PD 05-JUL-2001; 2001WO-EP007705.XX
PP 07-JUL-2000; 2000DE-01031080.XX
PR 19-APR-2001; 2001DE-01019294.XX
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.XX
PI Schaefer N, Scherl-Moatsgeer M, Sommergruber W, Abbeher R;XX
DR MPI; 2002-11704/22.XX
XX N-PSDB; ABA95507.XX
XX Claim 1; Page 85-86; 102pp; German.

This invention describes a novel tumour-associated antigen, designated B345 which has cytostatic activity. B345 is involved in communication, interaction and/or signal transduction with extracellular components and ligands, especially in the metastatic potential of cancer, particularly of the colon. B345 or its immunogenic fragments, also the DNA that encodes it, are useful for immunotherapy of cancer, particularly for carcinoma of lung or colon. Antibodies raised against B345 are useful for treatment and diagnosis of cancers that are associated with B345 expression, including their use for targeted delivery of cytotoxic or radioactive agents. Probes derived from B345 can be used to detect tumour-specific mutations in the B345 sequence, and can be used to screen for B345 specific modulators. This sequence represents a human B345 tumour-associated antigen described in the invention

XX
S0 Sequence 836 AA;

Query Match 99.8%; Score 4385; DB 5; Length 836;

Best Local Similarity 99.8%; Pred. No. 0;

Matches B345: Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MAGLNGCVSIALGVTLLQAAALPRGAPAPRIALPSSNTIVLIGFTLLAMPCTIYI 60

QY 61 SGRHITMLSIKSGRIYFTFSQSPENHFIIEIQKIDCKSGFCPPGEVQLQSTSLPT 120

DB 61 SGRHITMLSIKSGRIYFTFSQSPENHFIIEIQKIDCKSGFCPPGEVQLQSTSLPT 120

QY 121 LKRTITNVKAKHSGIGLELOPSIPRLROIGPGBSCPDGVTHSISGRIDATVVRIGTECSN 180

DB 121 LKRTITNVKAKHSGIGLELOPSIPRLROIGPGBSCPDGVTHSISGRIDATVVRIGTECSN 180

QY 181 GTVSRIKQCEVKAALHPFAPRANSGFSIANGSIRLCITISVFEGEGSATLMSANY 240

DB 181 GTVSRIKQCEVKAALHPFAPRANSGFSIANGSIRLCITISVFEGEGSATLMSANY 240

QY 241 PEGPPEDELTATQFVFAHLLASVSFLANFNSCERKEERYTIIIGSTTNPBYKLEDK 300

DB 241 PEGPPEDELTATQFVFAHLLASVSFLANFNSCERKEERYTIIIGSTTNPBYKLEDK 300

QY 301 OPGNAGNPLSLQGGCDQDQASPGILRLQFQVLRQHPONESNKIYVDLSNBRMSITIE 360

DB 301 OPGNAGNPLSLQGGCDQDQASPGILRLQFQVLRQHPONESNKIYVDLSNBRMSITIE 360

QY 361 PPRVQSKRPFGCPFCISRTCSNLTLSGSKHISFICDGLTRLMANVEKTI6CTDH 420

DB 361 PPRVQSKRPFGCPFCISRTCSNLTLSGSKHISFICDGLTRLMANVEKTI6CTDH 420

QY 421 RYCORRSYSLQVPSDILHLPVELHPSKELVPCORLSLYJPAQGLQOHHEKPCNTSF 480

DB 421 RYCORRSYSLQVPSDILHLPVELHPSKELVPCORLSLYJPAQGLQOHHEKPCNTSF 480

QY 481 SYLVASAIPSODLYFGSCFCGSGIKQIYVKNISVTLRTFAP9FRQBASROGLTVSP1PY 540

DB 481 SYLVASAIPSODLYFGSCFCGSGIKQIYVKNISVTLRTFAP9FRQBASROGLTVSP1PY 540

QY 541 PKEGVFTVTPDYSKYVLTPTMDRGLPSLTSVSNHISVPRQVACLPFPERSGVVCQ 600

DB 541 PKEGVFTVTPDYSKYVLTPTMDRGLPSLTSVSNHISVPRQVACLPFPERSGVVCQ 600

QY 601 TGRAPMIIQORTRAEZIFSLDEDLVLPKPSFPHHSFVWVINSNCSP7SGKQDLLESTLT 660

DB 601 TGRAPMIIQORTRAEZIFSLDEDLVLPKPSFPHHSFVWVINSNCSP7SGKQDLLESTLT 660

QY 661 PRTVDLTLLIANGCGVLLLSALGIIICVQKQKQKNGPANGIYNGNINTENPROPK 720

DB 661 PRTVDLTLLIANGCGVLLLSALGIIICVQKQKQKNGPANGIYNGNINTENPROPK 720

QY 721 KFORGRKNDSHVYVIEDTMYVGHLLQDSGSPLOPEVDIYRPFQGTWVCPPSPPTIC 780

DB 721 KFORGRKNDSHVYVIEDTMYVGHLLQDSGSPLOPEVDIYRPFQGTWVCPPSPPTIC 780

QY 781 SRAATATLATEBPSP 836

DB 781 SRAATATLATEBPSP 836

Search completed: May 4, 2006, 20:56:49
Job time : 190 secs

Fri May 5 16:14:27 2006

Exhibit B page 1 of 2

Page 1

GenCore version 5.1.7
Copyright (c) 1993 - 2006 BioCeleration Ltd.

OM protein - protein search, using bw model

Run on: May 4, 2006, 21:01:55 ; Search time 168 Seconds

(without alignments)
2079.198 Million cell updates/sec

Title: US-10-781-564-1
Perfect score: 4392
Sequence: 1 MAGLNCGVSIALLGVLLGA.....SSKTDIPILSTGEPMRPA 836

Scoring table: BLOSUM62
Gap 10.0, Gapext 0.5

Searched: 1867569 oego, 417829326 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 90%

Maximum Match 100%

Listing first 1000 summaries

Database: Published Applications AA_Main:
1: /cgn2_6/prodata/1/pubpa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubpa/US08_PUBCOMB.pep:*
3: /cgn2_6/prodata/1/pubpa/US09_PUBCOMB.pep:*
4: /cgn2_6/prodata/1/pubpa/US10_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubpa/US10B_PUBCOMB.pep:*
6: /cgn2_6/prodata/1/pubpa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4392	100.0	836	5 US-10-781-564-1	Sequence 1, Appli
2	4385	99.8	836	3 US-09-899-569A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-781-564-1
Sequence 1, Application US/10781564
Publication No. US20040247601A1
GENERAL INFORMATION:
APPLICANT: Onigley, James P.
APPLICANT: Hooper, John D.
APPLICANT: Teeter, Jacqueline E.
TITLE OF INVENTION: Methods for Diagnosing Cancer and Decreasing Metastasis by Cancer
FILE REFERENCE: 1361.036US1
CURRENT APPLICATION NUMBER: US/10/781,564
PRIOR APPLICATION NUMBER: 2004-02-18
PRIOR FILING DATE: 2003-02-19
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PACESEQ for Windows Version 4.0
SBO ID NO 1
LENGTH: 836
TYPE: PRT

ORGANISM: Homo sapiens
US-10-781-564-1
Query Match 100.0%; Score 4392; DB 5; Length 836;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 836; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAGLNCGVSIALLGVLLGAARIPRGAARIPRPSNTYLKLGTPYLAKCTIV 60
DB 1 MAGLNCGVSIALLGVLLGAARIPRGAARIPRPSNTYLKLGTPYLAKCTIV 60
QY 61 SRRHITLMSKSGERIVFTFSCSPENHFEIQRNIDCSGCPGEGVOLQPSLSPT 120
DB 61 SRRHITLMSKSGERIVFTFSCSPENHFEIQRNIDCSGCPGEGVOLQPSLSPT 120
QY 121 LRRFTIIVNKAHNSIGLQLQPSIPRLRQIGGCECPGQTHS1SGRIDATVVRIGTCSN 180
DB 121 LRRFTIIVNKAHNSIGLQLQPSIPRLRQIGGCECPGQTHS1SGRIDATVVRIGTCSN 180
QY 181 GTVSR1KMGECVKAALHLPMPHPRVSGPSIANKRSIKRLCIESEVFGESGATLMSANY 240
DB 181 GTVSR1KMGECVKAALHLPMPHPRVSGPSIANKRSIKRLCIESEVFGESGATLMSANY 240
QY 241 PGCPPEDELTMPQVVPYPAHLBASVSFLNPNLSNCRKEEVEVY1RGSTTPPEVPEL 300
DB 241 PGCPPEDELTMPQVVPYPAHLBASVSFLNPNLSNCRKEEVEVY1RGSTTPPEVPEL 300
QY 301 OPGNAGNFNLSLGGCDQDQSGILRLQFVLVQHPQNESNK1YVVDLSNERAMS171B 360
DB 301 OPGNAGNFNLSLGGCDQDQSGILRLQFVLVQHPQNESNK1YVVDLSNERAMS171B 360
QY 361 PRPVQSRKFPVCGFCVLSARCSNLTLSGSGHKSIFCDLRLWMNVEKTSCTDH 420
DB 361 PRPVQSRKFPVCGFCVLSARCSNLTLSGSGHKSIFCDLRLWMNVEKTSCTDH 420
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DB 421 RYCRKESYSLQVPSDILH1PYRLHDFSMKLVVPDRLSLV1PAQGLQOHTKPCNTSP 480
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DB 481 SYLVASAIIPSDLVFSGPCPGS1KQIOVKONISVTLRTFPAASPHQASRQGLTVSEIPY 540
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DB 541 FKRCGVPTVPTKSKVTLRTPMNRGLP1LTSVKNISVPRDOVALTPFKSSGVVCO 600
QY 601 TGRAFMIIOGQRTABE1FSLD2DYLPPSPHHS1FWVINSNCSPFSKQDL1FVTLT 660
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DB 661 PRYDLTYLIAVGGVLL1SALGLIICVKKKKKTKNGPAVG1YNGN1NTEMPROPK 720
QY 721 KQKGRKNDSHYAV1EDTNYGHLQDSGSLPQSDYTRPPQGTGVCPSPEPTIC 780
DB 721 KQKGRKNDSHYAV1EDTNYGHLQDSGSLPQSDYTRPPQGTGVCPSPEPTIC 780
QY 781 SRAPTAKLATEEPPSPSESESEPYTSHPNNDVSSKOTD1PL1STQEMERPAE 836
DB 781 SRAPTAKLATEEPPSPSESESEPYTSHPNNDVSSKOTD1PL1STQEMERPAE 836

/ TITLE OF INVENTION: Tumorigenicity Assay (B345)
 / FILE REFERENCE: 0652, 2280001
 / CURRENT APPLICATION NUMBER: US/09/899, 569A
 / CURRENT FILING DATE: 2001-07-06
 / PRIOR APPLICATION NUMBER: DE 100 33 080.0
 / PRIOR FILING DATE: 2000-07-07
 / PRIOR APPLICATION NUMBER: DE 101 19 294.0
 / PRIOR FILING DATE: 2001-04-19
 / PRIOR APPLICATION NUMBER: US 60/243,158
 / PRIOR FILING DATE: 2000-10-25
 / PRIOR APPLICATION NUMBER: US 60/297,747
 / PRIOR FILING DATE: 2001-06-14
 / NUMBER OF SEQ ID NOS: 40
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO: 4
 / LENGTH: 836
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 / US-09-899-569A-4

Query Match 99.8% Score 4385; DB 3; Length 836;
 Beat Local Similarity 99.8%; Pred. No. 0;

Matches 834; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGLNGVSIALLGTLGAAKLPKCAAEIALPESNITVLKLTPTLAKCYIVI 60
 DB 1 MAGLNGVSIALLGTLGAAKLPKCAAEIALPESNITVLKLTPTLAKCYIVI 60
 QY 61 SKHITMLSIKGERIVFTFSCSPENHPIETIIONIDMSGPCFGEVOLQSTSLPT 120
 DB 61 SKHITMLSIKGERIVFTFSCSPENHPIETIIONIDMSGPCFGEVOLQSTSLPT 120
 QY 121 LNTFTMDYKAKSKIGLELPSTPRLROIGPESCEPCGVTNLSGRIDATVRICTPCSN 180
 DB 121 LNTFTMDYKAKSKIGLELPSTPRLROIGPESCEPCGVTNLSGRIDATVRICTPCSN 180
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 DB 301 QGNAAGNPNLSLGGCDQNASPGILRLQFVTVQHPQNSNKIYYVDLSNERAMSLTIE 360
 QY 361 PRPVQSRKFPVPGCFVLESRTCSNLTLSGSKHISPLCDDLTMLNVEKTIISCTDH 420
 DB 361 PRPVQSRKFPVPGCFVLESRTCSNLTLSGSKHISPLCDDLTMLNVEKTIISCTDH 420
 QY 421 RYCORRYSLOVPSDILHLPVELHDSWKLVPKDRSLVLPVPAQLQOFTHEKPCNTSF 480
 DB 421 RYCORRYSLOVPSDILHLPVELHDSWKLVPKDRSLVLPVPAQLQOFTHEKPCNTSF 480
 QY 481 SYLVASALPSODLYFGSFCPCGSIKQIQVKNISVTLRTFAPSFRQBASRQCLTVSPIFY 540
 DB 481 SYLVASALPSODLYFGSFCPCGSIKQIQVKNISVTLRTFAPSFRQBASRQCLTVSPIFY 540
 QY 541 PKEGCVFTVPTDTSKAYLATPMNDRLPSLTSVSNISVPRDOVACLTFKERSGVVCO 600
 DB 541 PKEGCVFTVPTDTSKAYLATPMNDRLPSLTSVSNISVPRDOVACLTFKERSGVVCO 600
 QY 601 TGRAPMIOEORTAIEIISLDVTLPKCFSTHRSFVWNIISNCSPTSGKQLDLLFSVTLT 660
 DB 601 TGRAPMIOEORTAIEIISLDVTLPKCFSTHRSFVWNIISNCSPTSGKQLDLLFSVTLT 660
 QY 661 PRTVDLTVILIAVGGVLLLSALGLIICVQKGGKTKNGPAVGIYNGNINTEMPRPK 720
 DB 661 PRTVDLTVILIAVGGVLLLSALGLIICVQKGGKTKNGPAVGIYNGNINTEMPRPK 720
 QY 721 KFOKGRKNDSHVAVIEDTMVYGHLLQDSGSGFLQPEVDYTRPFGTNGVCPSPPTIC 780

DB 721 KFOKGRKNDSHVAVIEDTMVYGHLLQDSGSGFLQPEVDYTRPFGTNGVCPSPPTIC 780
 QY 781 SRAPTAKLATEPEPPSPRESSEBPTSHPNNDVSSQDTDIPULSTOEMPEPAE 836
 DB 781 SRAPTAKLATEPEPPSPRESSEBPTSHPNNDVSSQDTDIPULSTOEMPEPAE 836

Search completed: May 4, 2006, 21:05:31
 Job time: 168 secs

<!--StartFragment-->RESULT 1

Exhibit C

CDCP1_HUMAN

ID CDCP1_HUMAN STANDARD; PRT; 836 AA.
AC Q9H5V8; Q49UB4; Q6NT71; Q6U9Y2; Q8WU91; Q96QU7; Q9H676; Q9H8C2;
DT 07-MAR-2006, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2001, sequence version 1.
DT 07-MAR-2006, entry version 14.
DE CUB domain-containing protein 1 precursor (Transmembrane and
DE associated with src kinases) (Membrane glycoprotein gp140)
DE (Subtractive immunization M plus HEP3 associated 135 kDa protein)
DE (SIMA135) (CD318 antigen).
GN Name=CDCP1; Synonyms=TRASK; ORFNames=UNQ2486/PRO5773;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), VARIANT GLN-525, FUNCTION, AND
RP TISSUE SPECIFICITY.
RX MEDLINE=21359860; PubMed=11466621; DOI=10.1038/sj.onc.1204566;
RA Scherl-Mostageer M., Sommergruber W., Abseher R., Hauptmann R.,
RA Ambros P., Schweifer N.;
RT "Identification of a novel gene, CDCP1, overexpressed in human
RT colorectal cancer.";
RL Oncogene 20:4402-4408(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), N-GLYCOSYLATION,
RP PHOSPHORYLATION, SHEDDING, PROTEIN SEQUENCE OF 30-48; 281-293 AND
RP 427-438, GLYCOSYLATION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RX MEDLINE=22547370; PubMed=12660814; DOI=10.1038/sj.onc.1206220;
RA Hooper J.D., Zijlstra A., Aimes R.T., Liang H., Claassen G.F.,
RA Tarin D., Testa J.E., Quigley J.P.;
RT "Subtractive immunization using highly metastatic human tumor cells
RT identifies SIMA135/CDCP1, a 135 kDa cell surface phosphorylated
RT glycoprotein antigen.";
RL Oncogene 22:1783-1794(2003).
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), VARIANTS GLN-525 AND ASP-709,
RP IDENTIFICATION BY MASS SPECTROMETRY, PROTEIN SEQUENCE OF 30-34 AND
RP 369-375, PHOSPHORYLATION, GLYCOSYLATION, TISSUE SPECIFICITY, SUBUNIT,
RP AND FUNCTION.
RX PubMed=16007225; DOI=10.1038/sj.onc.1208582;
RA Bhatt A.S., Erdjument-Bromage H., Tempst P., Craik C.S., Moasser M.M.;
RT "Adhesion signaling by a novel mitotic substrate of src kinases.";
RL Oncogene 24:5333-5343(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2), AND VARIANT
RP GLN-525.

Exhibit C

RC TISSUE=Placenta;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3), AND NUCLEOTIDE
RP SEQUENCE [LARGE SCALE MRNA] OF 1-697 (ISOFORM 1).
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 1-691 (ISOFORM 1), IDENTIFICATION BY
RP MASS SPECTROMETRY, PHOSPHORYLATION, GLYCOSYLATION, AND TRYPTIC
RP CLIVAGE.
RC TISSUE=Epidermis;
RX PubMed=14739293; DOI=10.1074/jbc.M309678200;
RA Brown T.A., Yang T.M., Zaitsevskaja T., Xia Y., Dunn C.A., Sigle R.O.,

Exhibit C

RA Knudsen B., Carter W.G.;
 RT "Adhesion or plasmin regulates tyrosine phosphorylation of a novel
 RT membrane glycoprotein p80/gp140/CUB domain-containing protein 1 in
 RT epithelia.";
 RL J. Biol. Chem. 279:14772-14783(2004).
 RN [8]
 RP FUNCTION, AND PHOSPHORYLATION.
 RC TISSUE=Epidermis;
 RX MEDLINE=96178080; PubMed=8647901; DOI=10.1083/jcb.132.4.727;
 RA Xia Y., Gil S.G., Carter W.G.;
 RT "Anchorage mediated by integrin alpha6beta4 to laminin 5 (epiligrin)
 RT regulates tyrosine phosphorylation of a membrane-associated 80-kD
 RT protein.";
 RL J. Cell Biol. 132:727-740(1996).
 RN [9]
 RP FUNCTION.
 RX PubMed=12799299;
 RA Conze T., Lammers R., Kuci S., Scherl-Mostageer M., Schweifer N.,
 RA Kanz L., Buehring H.-J.;
 RT "CDCP1 is a novel marker for hematopoietic stem cells.";
 RL Ann. N. Y. Acad. Sci. 996:222-226(2003).
 RN [10]
 RP FUNCTION, AND TISSUE SPECIFICITY.
 RX PubMed=15153610;
 RA Buehring H.-J., Kuci S., Conze T., Rathke G., Bartolovic K.,
 RA Gruenebach F., Scherl-Mostageer M., Bruemmendorf T.H., Schweifer N.,
 RA Lammers R.;
 RT "CDCP1 identifies a broad spectrum of normal and malignant
 RT stem/progenitor cell subsets of hematopoietic and nonhematopoietic
 RT origin.";
 RL Stem Cells 22:334-343(2004).
 RN [11]
 RP IDENTIFICATION BY MASS SPECTROMETRY, INTERACTIONS WITH SRC AND PRKCG,
 RP AND MUTAGENESIS OF TYR-734 AND TYR-762.
 RX PubMed=15851033; DOI=10.1016/j.cell.2005.02.019;
 RA Benes C.H., Wu N., Elia A.E.H., Dharia T., Cantley L.C., Soltoff S.P.;
 RT "The C2 domain of PKCdelta is a phosphotyrosine binding domain.";
 RL Cell 121:271-280(2005).
 RN [12]
 RP IDENTIFICATION BY MASS SPECTROMETRY, AND FUNCTION.
 RX PubMed=16404722; DOI=10.1002/pmic.200500180;
 RA Andre M., Le Caer J.-P., Greco C., Planchon S., El Nemer W.,
 RA Boucheix C., Rubinstein E., Chamot-Rooke J., Le Naour F.;
 RT "Proteomic analysis of the tetraspanin web using LC-ESI-MS/MS and
 RT MALDI-FTICR-MS.";
 RL Proteomics 0:0-0(2006).
 CC -!- FUNCTION: May be involved in cell adhesion and cell matrix
 CC association. May play a role in the regulation of anchorage versus
 CC migration or proliferation versus differentiation via its
 CC phosphorylation. May be a novel marker for leukemia diagnosis and
 CC for immature hematopoietic stem cell subsets. Belongs to the
 CC tetraspanin web involved in tumor progression and metastasis.
 CC -!- SUBUNIT: Interacts with CDH2/N-cadherin, CDH3/P-cadherin,
 CC SDC1/syndecan-1, SDC4/syndecan-4 and the serine protease ST14/MT-
 CC SP1. Also interacts with SRC and PRKCG/protein kinase C gamma.
 CC -!- SUBCELLULAR LOCATION: Plasma membrane; single-pass membrane
 CC protein (Potential). Its shedding may lead to a soluble peptide.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=Q9H5V8-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9H5V8-2; Sequence=VSP_017432;
 CC Note=No experimental confirmation available;
 CC Name=3;

Exhibit C

CC IsoId=Q9H5V8-3; Sequence=VSP_017433, VSP_017434;
 CC Note=No experimental confirmation available;
 CC -!- TISSUE SPECIFICITY: Highly expressed in mitotic cells with low
 CC expression during interphase. Detected at highest levels in
 CC skeletal muscle and colon with lower levels in kidney, small
 CC intestine, placenta and lung. Expressed in a number of human tumor
 CC cell lines as well as in colorectal cancer, breast carcinoma and

Query Match 100.0%; Score 4392; DB 1; Length 836;
 Best Local Similarity 100.0%; Pred. No. 1.4e-312;
 Matches 836; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAGLNCGVSIALLGVLLGAARLPRGAFAFEIALPRESNITVLIKLGTPTLAKPCYIVI	60
Db	1	MAGLNCGVSIALLGVLLGAARLPRGAFAFEIALPRESNITVLIKLGTPTLAKPCYIVI	60
Qy	61	SKRHITMLSIKSGERIVFTFSCQSPENHFVIEIQKNIDCMGSPCFGEVQLQPSTSLPT	120
Db	61	SKRHITMLSIKSGERIVFTFSCQSPENHFVIEIQKNIDCMGSPCFGEVQLQPSTSLPT	120
Qy	121	LNRTFIWDVKAHKSIGLELQFSIPRLRQIGPGESCPDGVTHSISGRIDATVVRIGTFCSN	180
Db	121	LNRTFIWDVKAHKSIGLELQFSIPRLRQIGPGESCPDGVTHSISGRIDATVVRIGTFCSN	180
Qy	181	GTVSRIKMQEGVKMALHLPWFHPRNVSGFSIANRSSIKRLCIIESVFEGEGSATLMSANY	240
Db	181	GTVSRIKMQEGVKMALHLPWFHPRNVSGFSIANRSSIKRLCIIESVFEGEGSATLMSANY	240
Qy	241	PEGFPEDELMTWQFVVPALHRASVSFLNFNLSNCERKEERVEYYIPGSTTNPEVKLEDEK	300
Db	241	PEGFPEDELMTWQFVVPALHRASVSFLNFNLSNCERKEERVEYYIPGSTTNPEVKLEDEK	300
Qy	301	QPGNMAGNFNLSLQGCQDAQSPGILRLQFQVLVQHPQNESNKIYVVDLSNERAMSLTIE	360
Db	301	QPGNMAGNFNLSLQGCQDAQSPGILRLQFQVLVQHPQNESNKIYVVDLSNERAMSLTIE	360
Qy	361	PRPVKQSRKFVPGCFVCLESRTCSNLTLTSGSKHKISFLCDDLTRLWMNVEKTISCTDH	420
Db	361	PRPVKQSRKFVPGCFVCLESRTCSNLTLTSGSKHKISFLCDDLTRLWMNVEKTISCTDH	420
Qy	421	RYCQRKSYSLQVPSDILHLPVELHDFSWKLLVPKDRLSLVLVPAQKLQQTKEKPCNTSF	480
Db	421	RYCQRKSYSLQVPSDILHLPVELHDFSWKLLVPKDRLSLVLVPAQKLQQTKEKPCNTSF	480
Qy	481	SYLVASAIQSDLYFGSFCPGGSIKQIQVKQNISVTLRTFAPSFRQEASRQGLTVSFIPY	540
Db	481	SYLVASAIQSDLYFGSFCPGGSIKQIQVKQNISVTLRTFAPSFRQEASRQGLTVSFIPY	540
Qy	541	FKEEGVFTVTPDTKSKVYLRTPNWDRGLPSLTSVSWNISVPRDQVACLTFFKERSGVVCQ	600
Db	541	FKEEGVFTVTPDTKSKVYLRTPNWDRGLPSLTSVSWNISVPRDQVACLTFFKERSGVVCQ	600
Qy	601	TGRAFMIIQEQRTRAEEIFSLDEDVLPKPSFHHHSFWVNISNCSPTSGKQLDLLFSVTLT	660
Db	601	TGRAFMIIQEQRTRAEEIFSLDEDVLPKPSFHHHSFWVNISNCSPTSGKQLDLLFSVTLT	660
Qy	661	PRTVDLTVILIAAVGGGVLLLSALGLIICCVKKKKKKTNGKPAVGIYNGNINTEMPRQPK	720
Db	661	PRTVDLTVILIAAVGGGVLLLSALGLIICCVKKKKKKTNGKPAVGIYNGNINTEMPRQPK	720
Qy	721	KFQKGRKDNDSHVYAVIEDTMVYGHLLQDSSGSFLQPEVDTYRPFQGTMGVCPSPPTIC	780
Db	721	KFQKGRKDNDSHVYAVIEDTMVYGHLLQDSSGSFLQPEVDTYRPFQGTMGVCPSPPTIC	780
Qy	781	SRAPTAKLATEEPPPRSPPESESEPYTFSHPNNGDVSSKDTDIPLLSTQEPMEPAE	836

Db 781 SRAPTAKLATEEPPPRSPPESESEPYTFSHPNNGDVSSKDTDIPLLSTQEPMEPAE 836

Exhibit C

<!--EndFragment-->